Amendments to the Specification:

Please add the following section heading and paragraph after the title on page 1:

CROSS-REFERENCE TO RELATED APPLICATION

This application claims priority to U.S. Provisional Application Serial No. 60/425,532, filed November 12, 2002, incorporated herein by reference in its entirety.

Please replace the paragraph beginning at page 3, line 11, with the following amended paragraph:

The present invention relates to an isolated nucleic acid fragment encoding a PAIGB polypeptide selected from the group consisting ~~of:(a)~~ of: (a) an isolated nucleic acid fragment encoding SEQ ID ~~NO:2, 4 ,6 ,~~ NO: 2, 4, 6, 8 and 10, (b) an isolated nucleic acid fragment encoding an amino acid sequence having at least 85% identity with the SEQ ID NO: ~~2,4,6~~ 2, 4, 6, 8 and 10, (c) an isolated nucleic acid molecule that hybridizes with the isolated nucleic acid fragment of (a) under hybridization conditions of 6X SSC (1M NaCl), 45 to 50 % formamide, 1 % SDS at 37 °C, and a wash in 0.5X to 1X SSC at 55 to 60 °C; ~~and,(d)~~ and, (d) an isolated nucleic acid fragment that is complementary to (a), (b), or (c). The nucleic acid molecules and corresponding polypeptide fragments are contained in the accompanying sequence listing and described in Brief Description of the Invention.

Please replace the paragraph beginning on page 3, line 31, with the following amended paragraph:

In an alternate embodiment, the present invention provides methods of obtaining a nucleic acid fragment encoding the PAIGB polypeptide ~~comprising:(a)probing~~ comprising: (a) probing a genomic library with all or a portion of a nucleic acid fragment as set forth in SEQ ID ~~NO:3;(b)identifying~~ NO:3; (b) identifying a DNA clone that hybridizes with the nucleic acid fragment of step (a); and

determining the sequence of the nucleic acid fragment that comprises the DNA clone identified in step (b).

Please replace the paragraph beginning on page 20, line 11, with the following amended paragraph:

The polynucleotides may be flanked by natural regulatory (expression control) sequences, or may be associated with heterologous sequences, including promoters, internal ribosome entry sites (IRES) and other ribosome binding site sequences, enhancers, response elements, suppressors, signal sequences, polyadenylation sequences, introns, 5'- and 3'-non-coding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, “caps”, substitution of one or more naturally occurring nucleotides with an analog, and internucleotide modifications such as, for example, those with uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates~~, etc~~) and with charged linkages (*e.g.*, phosphorothioates, phosphorodithioates~~, etc.~~). Polynucleotides may contain one or more additional covalently linked moieties, such as, for example, proteins (*e.g.*, nucleases, toxins, antibodies, signal peptides, poly-L-lysine~~, etc.~~), intercalators (*e.g.*, acridine, psoralen~~, etc.~~), chelators (*e.g.*, metals, reactive metals, iron, oxidative metals~~, etc.~~), and alkylators. The polynucleotides may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the polynucleotides herein may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

Please replace the paragraph beginning on page 21, line 9, with the following amended paragraph:

A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as cDNA, genomic DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and solution ionic strength (Sambrook, J. et al. eds., *Molecular Cloning: A Laboratory Manual* (2d Ed. 1989) Cold Spring Harbor Laboratory Press, NY. Vols. 1-3 (ISBN 0-87969-309-6)). The conditions of temperature and ionic strength determine the "stringency" of the hybridization. For preliminary screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a T_m of ~~55°~~ 55 °C, can be used, *e.g.*, 5x SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30% formamide, 5x SSC, 0.5% SDS). Moderate stringency hybridization conditions correspond to a higher T_m, *e.g.*, 40% formamide, with 5x or 6x ~~SCC~~ SSC. High stringency hybridization conditions correspond to the highest T_m, *e.g.*, 50% formamide, 5x or 6x ~~SCC~~ SSC. Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating T_m have been derived (Sambrook et al. eds., *Molecular Cloning: A Laboratory Manual* (2d Ed. 1989) Cold Spring Harbor Laboratory Press, NY. Vols. 1-3 (ISBN 0-87969-309-6), 9.50-9.51). For hybridization with shorter nucleic acids, *i.e.*, oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (Sambrook et al. eds., *Molecular Cloning: A Laboratory Manual* (2d Ed. 1989) Cold Spring Harbor Laboratory Press, NY. Vols. 1-3 (ISBN 0-87969-309-6) 11.7-11.8).